

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: March 14, 2003, 02:07:45 ; Search time 92.2921 Seconds

(without alignments)
1579.326 Million cell updates/sec

Title: US-09-698-781-17
Perfect score: 44
Sequence: 1 TLFPVLFL 9

Scoring table:

BLOSUM62
Xgapop 10.0, Ygapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1615406 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL-frame+ .p2n.model -DEV-xlh
-O/cgn2_1/USPto.spool/US09698781/runat_07032003_083459_5329/app.query.fasta.1.654
-DB-EST -QFMT-fastap -SUFFIX-p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX-biosum62 -TRANS-human40.cdi -LIST=45
-DOCLALIGN=200 -THR SCORE-pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT-pio -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09698781 -GCN.1.1_2463 -runat_07032003_083459_5329 -NCPU=6 -ICPU=3
-NO_XLPAY -NO_MMAP -LARGEQUERY -NEC_SCORES=0 -WAIT -LONGLOG -DEV-TIMEOUT=120
-WARN-TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	547 9	AL703262	AL703262 DKF2p686K
2	42	95.5	353 14	BQ666605	BQ666605 OHB27R16
3	41	93.2	308 14	BM832007	BM832007 K-EST0106
4	41	93.2	407 14	BM822727	BM822727 K-EST0092
5	41	93.2	447 10	AM009767	AM009767 w87b09.x
6	41	93.2	461 10	BB839116	BB839116 BB839116
7	41	93.2	538 14	BM751298	BM751298 K-EST0027
8	41	93.2	575 10	BE036163	BE036163 MO20E02 M
9	41	93.2	619 17	A2108486	A2108486 RPT-23-4
10	41	93.2	693 9	AU138699	AU138699 AU138699
11	41	93.2	722 12	BG718279	BG718279 602696263
12	41	93.2	724 10	BE545083	BE545083 601077815
13	41	93.2	767 13	BM013479	BM013479 603638933
14	41	93.2	785 14	BM715733	BM715733 UT-E-EG0-
15	41	93.2	813 12	BG574770	BG574770 602596822
16	41	93.2	861 14	BQ441085	BQ441085 AGENCOURT
17	41	93.2	869 17	A2539955	A2539955 ENTES35TF
18	41	93.2	898 17	A2666486	A2666486 ENTMA76TF
19	41	93.2	921 17	BH132102	BH132102 ENTPB47TF
20	41	93.2	972 14	BQ068805	BQ068805 AGENCOURT
21	41	93.2	1018 14	BQ071051	BQ071051 AGENCOURT
22	41	93.2	1072 14	BQ052048	BQ052048 AGENCOURT
23	41	93.2	1075 14	BQ069622	BQ069622 AGENCOURT
24	41	93.2	1094 12	BG118306	BG118306 602350108
25	41	93.2	1117 10	BE372269	BE372269 601223588
26	41	93.2	1187 17	A2686289	A2686289 ENTKU74TF
27	40	90.9	349 13	B1178406	B1178406 EST519351
28	40	90.9	421 10	BE177732	BE177732 RC1-H7059
29	40	90.9	469 17	AQ209341	AQ209341 HS_3240_A
30	40	90.9	578 17	A2848527	A2848527 2M0151C06
31	40	90.9	643 14	BQ120863	BQ120863 EST606439
32	40	90.9	656 14	BQ505928	BQ505928 EST617043
33	40	90.9	659 10	BB344289	BB344289 EST617043
34	40	90.9	955 17	CNS0701T	A4323675 T3 end of
35	39	88.6	103 9	A1956273	A1956273 u173b11.y
36	39	88.6	105 17	A2828001	A2828001 2M0104F13
37	39	88.6	186 9	A1572293	A1572293 te39d11.x
38	39	88.6	192 12	BF819364	BF819364 IL0-RT001
39	39	88.6	270 17	TA383B01Q	AL497965 T. brucei
40	39	88.6	297 17	B82165	B82165 RPII11-26D7
41	39	88.6	309 12	BF331555	BF331555 RCO-BT056
42	39	88.6	318 12	BF879720	BF879720 RC2-ET018
43	39	88.6	334 9	AA883350	AA883350 a145c10.s
44	39	88.6	340 9	AA007134	AA007134 13CDNA93-
45	39	88.6	342 10	BB870337	BB870337 BB870337

ALIGNMENTS

RESULT 1	AL703262	547 bp	mRNA	linear	EST 22-MAR-2002
LOCUS	AL703262				
DEFINITION	DKF2p686K1819_r1 686 (synonym: hlc3) Homo sapiens cDNA clone				
ACCESSION	AL703262.1				
VERSION	AL703262.1				
KEYWORDS	GI:19686617				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 547)				
	Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).				
	EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann				

JOURNAL
COMMENT

Unpublished (1999)
Contact: Poustka A.J.
Department Lehnach
Max-Planck-Institute for Molecular Genetics
Inhestrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-84131128

Email: poustka@mpg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 5' sequence available.
This clone (DKFZp686K1819) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source

1..547
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp686K1819"
/clone_lib="686 (synonym: h1cc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTRIPlex2; Site_1: SfilA; Site_2: SfilB;
cDNA collection"

BASE COUNT
ORIGIN

170 a 120 c 120 g 137 t

Alignment Scores:

Pred. No.: 373
Score: 44.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%

Length: 547
Matches: 9
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-698-781-17 (1-9) x AL703262 (1-547)

OY 1 ThirleupheProValleuleuPhelu 9
|||||
Db 46 ACATTATTCACAGCTGCTTCTCTG 72

RESULT 2

BQ966605/c

LOCUS BQ966605 353 bp mRNA linear EST 21-AUG-2002
DEFINITION QHB27F16, yg ab1 QH.ABCDI sunflower RHA801 Helianthus annuus cDNA
clone QHB27F16, mRNA sequence.

ACCESSION BQ966605
VERSION BQ966605.1 GI:22383710
KEYWORDS EST.
SOURCE common sunflower.
ORGANISM Helianthus annuus

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; easterids II; Asterales; Asteraceae; Asteroidae;
Heliantheae; Helianthus.

REFERENCE
AUTHORS

1 (bases 1 to 353)
Kozik A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison,
P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)

JOURNAL
COMMENT

Contact: Alexander Kozik [R.W.Michelmore]
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University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA

Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@ucdavis.edu]
Singleton, see http://cgpbdb.ucdavis.edu/ for details.
Plate: QHB27 row: F column: 16.
Location/Qualifiers
1..353

FEATURES
source

/organism="Helianthus annuus"
/cultivar="RHA801"
/db_xref="taxon:4232"
/clone="QHB27F16"
/clone_lib="QH.ABCDI sunflower RHA801"
/lab_host="E.coli"
/note="Vector: pBRCDNA5flab: The library was constructed
from 11 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpbdb.ucdavis.edu/
TAG_LIB-QH.ABCDI sunflower RHA801
TAG_TISSUE=roots
TAG_SEQ=GTTCACGCGC"

BASE COUNT
ORIGIN

104 a 58 c 95 g 96 t

Alignment Scores:

Pred. No.: 494
Score: 42.00
Percent Similarity: 100.00%
Best Local Similarity: 88.89%
Query Match: 95.45%

Length: 353
Matches: 8
Conservative: 1
Mismatch: 0
Indels: 0
Gaps: 0

US-09-698-781-17 (1-9) x BQ966605 (1-353)

OY 1 ThirleupheProValleuleuPhelu 9
|||||
Db 217 ACTATTTTCCCGCTCTTCTCTCTT 191

RESULT 3

BM832007/c

LOCUS BM832007 308 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0106159 520T665307 Homo sapiens cDNA clone 520T665307-32-C08
5', mRNA sequence.

ACCESSION BM832007
VERSION BM832007.1 GI:19188416
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 308)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

REFERENCE
AUTHORS

Kim, Y.S.
ZIC Frontiers Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@kribb.re.kr
Plate: 32 row: C column: 08
High quality sequence stop: 308.

FEATURES
source

1..308
/organism="Homo sapiens"
/db_xref="taxon:9606"

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/clone-"S20T665307-32-C08"
/clone.lib-"S20T665307"
/sex-"M"
/lab_host-"Top10F"
/Note-"Organ: Stomach; Vector: pcNS; Site_1: ECORI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tabacco acid pyrophosphatase (TAP). The deapped
Intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT      117 a      54 c      99 g      38 t
ORIGIN

Alignment Scores:
Pred. No.:      629      Length:      308
Score:          41.00     Matches:      8
Percent Similarity: 100.00%  Conservative: 1
Best Local Similarity: 88.89%  Mismatches:  0
Query Match:    93.18%     Indels:      0
DB:             14        Gaps:        0

US-09-698-781-17 (1-9) x BM832007 (1-308)

Qy      1  ThrleupheProvalleuLeupheleu 9
|||||
Db      133 ACTCTCTTCTCTCTCTCTTCTTCTT 107

RESULT 4
BM822727/c      407 bp      mRNA      linear      EST 06-MAR-2002
LOCUS          K-EST0092951 S20T665307 Homo sapiens CDNA clone S20T665307-17-H07
DEFINITION     5', mRNA sequence.
ACCESSION     BM822727
VERSION       BM822727.1 GI:19179140
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 407)
AUTHORS       Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
               Kim,K.U., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
               Kim,Y.S.
TITLE          21C Frontier Korean EST Project 2001
JOURNAL        Unpublished (2002)
COMMENT        Contact: Kim YS
               Genome Research Center
               Korea Research Institute of Bioscience & Biotechnology
               52 Eoen-dong Yuseong-gu, Daejeon 305-333, South Korea
               Tel: +82-42-860-4470
               Fax: +82-42-860-4409
               Email: yongsung@mail.kribb.re.kr
               Plate: 17 row: H column: 07
               High quality sequence stop: 407.
               Location/Qualifiers
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               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone-"S20T665307-17-H07"
               /clone.lib-"S20T665307"
               /sex="M"
               /lab_host-"Top10F"
               /Note-"Organ: Stomach; Vector: pcNS; Site_1: ECORI;

```

```

               Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
               bacterial alkaline phosphatase (BAP) and then deapped
               with tabacco acid pyrophosphatase (TAP). The deapped
               Intact mRNA was ligated with DNA-RNA linker including EcoR
               I site by treatment of T4 RNA ligase and the first strand
               cDNA was synthesized from oligo dt-selected mRNA by
               priming with dt-tailed vector. The dt-tailed vector was
               adjusted to have about 60nt. The cDNA vector was
               circularized with E. coli DNA ligase after digestion of
               EcoRI which site is also included in vector. An RNA strand
               converted to a DNA strand by Okayama-Berg method. The
               obtained cDNA vectors were used for transformation of
               competent cells E. coli Top10F by electroporation method.
               The cDNA libraries constructed by this method are
               full-length enriched cDNA library."

BASE COUNT      132 a      85 c      129 g      61 t
ORIGIN

Alignment Scores:
Pred. No.:      889      Length:      407
Score:          41.00     Matches:      8
Percent Similarity: 100.00%  Conservative: 1
Best Local Similarity: 88.89%  Mismatches:  0
Query Match:    93.18%     Indels:      0
DB:             14        Gaps:        0

US-09-698-781-17 (1-9) x BM822727 (1-407)

Qy      1  ThrleupheProvalleuLeupheleu 9
|||||
Db      71 ACTCTTCTCTCTCTCTTCTTCTT 45

RESULT 5
AM009767/c      447 bp      mRNA      linear      EST 10-SEP-1999
LOCUS          W887B09.X1 NCI_CGAP_C03 Homo sapiens CDNA clone IMAGE:2504921 3',
DEFINITION     RNA sequence.
ACCESSION     AM009767
VERSION       AM009767.1 GI:5858545
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 447)
AUTHORS       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
               Unpublished (1997)
JOURNAL        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs@mail.nih.gov
               Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.,
               Ph.D.
TITLE          CDNA Library Preparation: M. Bento Soares, Ph.D.
               CDNA Library Arraying: Greg Lennon, Ph.D.
               DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/ULNL at:
               www.bio.lnll.gov/btrp/image/image.html
               Seq primer: -40UP from Gibco.
               Location/Qualifiers
               1..447
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone-"IMAGE:2504921"
               /clone.lib-"NCI_CGAP_C03"
               /sex="pooled"
               /tissue_type="colon"
               /lab_host-"DH10B"
               /Note-"Vector: p77T3D-Pac (Pharmacia) with a modified
               polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
               was prepared from 12 pooled bulk tumor samples and primed
               with a Not I - oligo(dt) primer. Double-stranded cDNA was

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ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTZ19 vector. Library went through one round of normalization. "

BASE COUNT 171 a 67 c 139 t

ALIGNMENT SCORES:

Pred. No.: 998 Length: 447
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 93.18% Indels: 0
DB: 10 Gaps: 0

US-09-698-781-17 (1-9) x AM009767 (1-447)

Oy 1 Thirleupheovalleupheleu 9

Db 332 ACCTGTTTCCTTATTTATTTCTG 306

RESULT 6

BB839116/c

LOCUS BB839116 461 bp mRNA linear EST 21-NOV-2001
DEFINITION BB839116 RIKEN full-length enriched, 8 cells embryo Mus musculus
CDNA clone E860007012 5', mRNA sequence.

ACCESSION BB839116

VERSION BB839116.1 GI:17039847

KEYWORDS EST.

SOURCE

ORGANISM

Mus musculus

house mouse.

REFERENCE

AUTHORS

1 (bases 1 to 461)
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Eutelestomi:
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eutelestomi:
Akimura, T., Akakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hirose, K., Hirose, T., Imotani, K., Ishii,
Y., Ito, M., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa,
A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watanabe, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length CDNAs (Akimura, T., et al.
2001)

Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh

, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wgk, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura

, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and

Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara

, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for

FEATURES

source

e mouse tissues.

Location/Qualifiers

1..461

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="E860007012"

/clone_lib="RIKEN full-length enriched, 8 cells embryo"

/cell_type="8 cells"

/dev_stage="8 cells embryo"

/note="Vector: pSPORI1. Site1: SalI. Site2: NotI. This

clone is among a rearranged set of 15,247 clones from 11

embryo cDNA libraries (including preimplantation stage

embryos from unfertilized egg to blastocyst, embryonic

part of E7.5 embryos, extraembryonic part of E7.5 embryos

, and E12.5 female mesonephros/gonad) and one newborn

ovary cDNA library. Average insert size 1.5 kb. All

source libraries are cloned unidirectionally with Oligo(dT

)Not primers. References include: (1) Genome-wide

expression profiling of mid-gestation placenta and embryo

using a 15,000 mouse developmental cDNA microarray, 2000,

Proc. Natl. Acad. Sci. U.S.A. 97: 9127-9132. (2)

Large-scale cDNA analysis reveals phased gene expression

patterns during preimplantation mouse development, 2000,

Development, 127: 1737-1749; (3) Genome-wide mapping of

unselected transcripts from extraembryonic tissue of

7.5-day mouse embryos reveals enrichment in the t-complex

and under-representation on the X chromosome, 1998, Hum

Mol. Genet. 7: 1967-1978."

Mol. Genet. 7: 1967-1978."

BASE COUNT 158 a 74 c 83 g 146 t

ORIGIN

Alignment Scores:

Pred. No.: 1.04e+03 Length: 461
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 93.18% Indels: 0
DB: 10 Gaps: 0

US-09-698-781-17 (1-9) x BB839116 (1-461)

Oy 1 Thirleupheovalleupheleu 9

Db 198 ACTCTTTTCCACGCTCTTCTC 172

RESULT 7

BM751298/c

LOCUS BM751298 538 bp mRNA linear EST 04-MAR-2002

DEFINITION K-EST0027248 S9SNUG01 Homo sapiens cDNA clone S9SNUG01-12-H12 5',

mRNA sequence.

ACCESSION BM751298

VERSION BM751298.1 GI:19080916

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eutelestomi;

Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.

1 (bases 1 to 538)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Oh, K.T., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsungem@kribb.re.kr

Plate: 12 row: H column: 12

High quality sequence stop: 538.

FEATURES
SOURCE

Location/Qualifiers
1. 538
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S9SNU601-12-H12"
/clone_lib="S9SNU601"
/sex="M"
/tissue_type="Ascites"
/cell_type="Epithelial"
/cell_line="SNU-601"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pME18-FL3; Site:1: XhoI;
Site:2: XhoI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAR) and then deacapped
with tabacco acid pyrophosphatase (TAP). The deacapped
intact mRNA was ligated with DNA-RNA linker including SfiI
site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Superscript II using SfiI
oligo-dT primer. After first strand synthesis, RNA was
degraded by NaOH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with SfiI and
cloned into DraIII- digested pME18-FL3 vector. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT
ORIGIN

196 a 104 c 102 g 136 t

Alignment Scores:

Pred. No.: 1.26e+03 Length: 538
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 86.89% Mismatches: 0
Query Match: 93.18% Indels: 0
DB: 14 Gaps: 0

US-09-698-781-17 (1-9) x BM751298 (1-538)

OY 1 ThrLeuphProValleuLeuphLeu 9
|||||
DB 48 ACGTGTTCGCGCTCTCTTTCTG 22

RESULT 8
BE036163

LOCUS BE036163 575 bp mRNA linear EST 07-JUN-2000
DEFINITION MO20E02 MO Mesembryanthemum crystallinum cDNA 5', mRNA sequence.
ACCESSION BE036163
VERSION BE036163.1 GI:8331172
KEYWORDS EST

SOURCE
ORGANISM

Common Iceplant.
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 575)

REFERENCE
AUTHORS

Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferreira,
H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio, C.,
Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: chm@u.arizona.edu.

TITLE
JOURNAL

Unpublished (2000)

Contact: Michalowski, C.B.

University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: chm@u.arizona.edu.

FEATURES
source

Location/Qualifiers
1. 575
/organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/clone_lib="MO"
/tissue_type="apical meristem and leaf primordia"

/dev_stage="5 weeks"
/note="no stress"
BASE COUNT 150 a 109 c 117 g 199 t
ORIGIN

Alignment Scores:

Pred. No.: 1.36e+03 Length: 575
Score: 41.00 Matches: 7
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 77.78% Mismatches: 0
Query Match: 93.18% Indels: 0
DB: 10 Gaps: 0

US-09-698-781-17 (1-9) x BE036163 (1-575)

OY 1 ThrLeuphProValleuLeuphLeu 9
|||||
DB 157 ACCCTGTCCGCTATTTGATCTCTTA 183

RESULT 9
A2108486

LOCUS A2108486 619 bp DNA linear GSS 09-MAY-2000
DEFINITION RPCI-23-469G20.TJB RPCI-23 Mus musculus genomic clone
ACCESSION RPCI-23-469G20, DNA sequence.
VERSION A2108486
KEYWORDS A2108486.1 GI:7761463
GSS.

SOURCE
ORGANISM

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 619)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akhurst,
B., Levins, M., Megam, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-469G20.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

TITLE
JOURNAL

Unpublished (1999)
Other GSSs: RPCI-23-469G20.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)
or from Resea ch Genetics (http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html)
Plate: 469 row: 6 column: 20
Seq primer: Sp6
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1. 619
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-469G20"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site:1:
EcoRI; Site:2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT
ORIGIN

167 a 150 c 105 g 197 t

Alignment Scores:

Pred. No.:	1.49e+03	Length:	619
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	88.89%	Mismatches:	0
Query Match:	93.18%	Indels:	0
DB:	17	Gaps:	0

US-09-698-781-17 (1-9) x AZ108486 (1-619)

QY 1 ThirleupheProvalleuLeupheleu 9

DB 452 ACCCTCTCCCTCTCTCTCTCTCTC 478

RESULT 10

AU138699/c

LOCUS AU138699 693 bp mRNA linear EST 02-AUG-2002

DEFINITION AU138699 PLACEL Homo sapiens CDNA clone PLACE1009120 5', mRNA

ACCESSION

AU138699

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1

Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and

Isogai, T.

HRI human CDNA project

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomeshri.co.jp

HRI human CDNA project: 5'-6 3'-end one pass sequencing: Helix

Research Institute; CDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

Location/Qualifiers

1. .693

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="PLACE1009120"

/clone_id="PLACE1"

/tissue-type="Placenta"

/note="Vector: PME18SFL3"

BASE COUNT 261 a 124 c 141 g 164 t 3 others

ORIGIN

Alignment Scores:

Pred. No.:

1.72e+03

Score:

41.00

Percent Similarity:

100.00%

Best Local Similarity:

88.89%

Query Match:

93.18%

DB:

9

Gaps:

0

US-09-698-781-17 (1-9) x AU138699 (1-693)

QY 1 ThirleupheProvalleuLeupheleu 9

DB 238 ACCTGTTCCGCTCTCTCTCTCTCTG 212

RESULT 11

BG718279/c

LOCUS BG718279 722 bp mRNA linear EST 08-MAY-2001

DEFINITION BG718279 722 bp mRNA linear EST 08-MAY-2001

602696263F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:4828598 5',

mRNA sequence.

ACCESSION BG718279

VERSION BG718279.1 GI:13997466

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 722)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NMGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

plate: LLM10746 row: m column: 15

High quality sequence stop: 718.

Location/Qualifiers

1. .722

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4828598"

/clone_id="NIH_MGC_97"

/lab_host="DH10B"

/note="Organ: testis; Vector: pBluescript (modified

pBluescript KS+); site.1: BamHI; site.2: SalI-XhoI (gtcgag

); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTT-3',

size selected for average insert size 2.2 kb and

normalized to ROP 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NMGRI, National

Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 261 a 139 c 151 g 171 t

ORIGIN

Alignment Scores:

Pred. No.:

1.81e+03

Score:

41.00

Percent Similarity:

100.00%

Best Local Similarity:

88.89%

Query Match:

93.18%

DB:

12

Gaps:

0

US-09-698-781-17 (1-9) x BG718279 (1-722)

QY 1 ThirleupheProvalleuLeupheleu 9

DB 200 ACCTGTTCCGCTCTCTCTCTCTCTG 174

RESULT 12

BE545083/c

LOCUS BE545083 724 bp mRNA linear EST 09-AUG-2000

DEFINITION BE545083 724 bp mRNA linear EST 09-AUG-2000

601077815F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:3463851 5',

mRNA sequence.

ACCESSION BE545083

VERSION BE545083

KEYWORDS BE545083.1 GI:9773728

SOURCE EST.

ORGANISM human.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 724)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHM8463 row: m column: 04
 High quality sequence stop: 689.
 Location/Qualifiers

FEATURES

source

1..724
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3463851"
 /clone_lib="NIH_MGC_12"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /note="Organ: cervix; Vector: PCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."
 Technology:

BASE COUNT 257 a 131 c 164 g 172 t
 ORIGIN

Alignment Scores:

Pred. No.: 1.81e+03 Length: 724
 Score: 41.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 88.89% Mismatches: 0
 Query Match: 93.18% Indels: 0
 DB: 10 Gaps: 0

US-09-698-781-17 (1-9) x BE545083 (1-724)

Oy 1 ThrlaupheProvalleuLeuphelen 9

Db 359 ACCTGTTCCGCTTCTTCTTCTTCTG 333

RESULT 13

BM013479/c

LOCUS 603638933p1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5415056 5',
 DEFINITION mRNA sequence.

ACCESSION BM013479 GI:16527833

VERSION BM013479.1 GI:16527833

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 767)
 NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHM12059 row: a column: 09
 High quality sequence stop: 767.
 Location/Qualifiers

FEATURES

source

1..767
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5415056"
 /clone_lib="NIH_MGC_87"
 /tissue_type="mammary adenocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"
 /note="Organ: breast; Vector: PCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.383 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."
 Technology:

BASE COUNT 237 a 174 c 207 g 149 t
 ORIGIN

Alignment Scores:

Pred. No.: 1.95e+03 Length: 767
 Score: 41.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 88.89% Mismatches: 0
 Query Match: 93.18% Indels: 0
 DB: 13 Gaps: 0

US-09-698-781-17 (1-9) x BM013479 (1-767)

Oy 1 ThrlaupheProvalleuLeuphelen 9

Db 62 ACTCTTCTCCTCTTCTTCTTCTTCTT 36

RESULT 14

BM715733/c

LOCUS 785 bp mRNA linear EST 28-FEB-2002
 DEFINITION UT-E-EJ0-ahj-o-03-0-UI r2 UI-E-EJ0 Homo sapiens cDNA clone

ACCESSION BM715733

VERSION BM715733.1 GI:19028991

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 785)

AUTHORS

TITLE

JOURNAL

COMMENT

discovery
 genome Res. 6 (9), 791-806 (1996)
 9704447
 Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msquares@blue.weeg.uiowa.edu
 Tissue Procurement: Dr. Gregg Hagaman
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 The following repetitive elements were found in this cDNA
 sequence: 254-301, >(GAA)n#Simple-repeat
 Seq primer: M13 Reverse.

FEATURES

source

1..785
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UT-E-EJ0-ahj-o-03-0-UI"
 /clone_lib="UI-E-EJ0"
 /tissue_type="fetal eyes, lens, eye anterior segment,
 optic nerve, retina, Retina Foveal and Macular, RPE and
 Choroid"
 /dev_stage="fetal and adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 UI-E-EJ0 is a subtracted cDNA library constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGATCAGAGA; lens, CGATTAGCGA; eye anterior segment, ATGCCGAT; optic nerve, CCATTAGTG; retina, CCGCG; Retina foveal and Macular, GTCC; RPE and Choroid, ACCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 254 a 185 c 227 g 116 t 3 others

Alignment Scores:

Pred. No.: 2.01e+03 Length: 785
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 93.18% Indels: 0
DB: 14 Gaps: 0

US-09-698-781-17 (1-9) x BM715733 (1-785)

OY 1 ThrlaupheprovalleuLeuphela 9

DB 287 ACCTCTTTCCTCTCTCTCTTTCCT 261

RESULT 15

BG574770/c 813 bp mRNA linear EST 10-APR-2001
LOCUS 60259682F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4705665 5',
DEFINITION mRNA sequence.

ACCESSION BG574770 GI:13582423

VERSION BG574770.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: c9apbs-remail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LHAM10572 row: 1 column: 06

High quality sequence stop: 801.

Location/Qualifiers

1. 813

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4705685"

/clone_1lb="NIH_MGC_87"

/tissue_type="mammary adenocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: breast; Vector: PCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.383 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."

BASE COUNT 247 a 180 c 223 g 163 t

ORIGIN

Alignment Scores:

Pred. No.: 2.09e+03 Length: 813
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 93.18% Indels: 0
DB: 12 Gaps: 0

US-09-698-781-17 (1-9) x BG574770 (1-813)

OY 1 ThrlaupheprovalleuLeuphela 9

DB 31 ACCTCTTTCCTCTCTCTTTCCT 5

Search completed: March 14, 2003, 05:26:20
Job time: 97.2921 secs